

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

(i) APPLICANT: Bandman, Olga  
 Lal, Preeti  
 Guegler, Karl J.  
 Shah, Purvi  
 Corley, Neil C.

(ii) TITLE OF THE INVENTION: VESICLE TRAFFICKING PROTEINS

(iii) NUMBER OF SEQUENCES: 9

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 (B) STREET: 3174 Porter Dr.  
 (C) CITY: Palo Alto  
 (D) STATE: CA  
 (E) COUNTRY: USA  
 (F) ZIP: 94304

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
 (B) COMPUTER: IBM Compatible  
 (C) OPERATING SYSTEM: DOS  
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
 (B) FILING DATE: Filed Herewith

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:  
 (B) FILING DATE:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.  
 (B) REGISTRATION NUMBER: 36,749  
 (C) REFERENCE/DOCKET NUMBER: PF-0417 US

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555  
 (B) TELEFAX: 650-845-4166

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 570 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: THPIPEB01  
 (B) CLONE: 75871

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Asn	Val	Val	Phe	Ala	Val	Lys	Gln	Tyr	Ile	Ser	Lys	Met	Ile	Glu
1				5				10						15	
Asp	Ser	Gly	Pro	Gly	Met	Lys	Val	Leu	Leu	Met	Asp	Lys	Glu	Thr	Thr
			20					25						30	

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## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THPIPEB01
- (B) CLONE: 75871

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGACCTCGCG	TCGGGCCAAC	AGACTGCGGG	GTTAATTTAG	CCAGACACGT	GGGCGGGAAG	60
GGCTGTAGGG	TACTTGTCAA	TTCGCCGCCA	TGAACGTGGT	TTTTGCTGTG	AAGCAGTACA	120
TTTCCAAAT	GATAGAGGAC	AGCGGGCCTG	GTATGAAAGT	ACTTCTCATG	GATAAAGAGA	180
CGACTGGCAT	AGTGAGTATG	GTATACACAC	AATCGGAGAT	TCTACAGAAG	GAAGTGTAAC	240
TCTTTGAACG	CATCGATTCT	CAAAATCGAG	AGATCATGAA	ACACCTGAAG	GCAATTTGTT	300
TTCTTCGACC	TACAAAGGAG	AATGTGGATT	ATATTATTCA	GGAGCTCCGA	AGACCCAAAT	360
ACACTATATA	TTTCATTTAT	TTCAGTAATG	TGATCAGCAA	GAGTGACGTG	AAGTCATTGG	420
CTGAAGCTGA	TGAACAGGAA	GTTGTGGCTG	AGGTTTCAGG	ATTTTATGGT	GATTACATTG	480
CTGTGAACCC	ACATTTGTTT	TCCCTCAATA	TTTTGGGTTG	CTGCCAGGGT	CGAAATTGGG	540
ATCCAGCCCA	GCTATCTAGA	ACAACCTAAG	GGCTTACAGC	TCTCCTTTTA	TCTCTGAAGA	600
AGTGTCCCAT	GATTCGTTAT	CAGCTCTCAT	CAGAGGCAGC	AAAGAGACTT	GCAGAGTGCG	660
TTAAGCAAGT	GATAACTAAA	GAATATGAAC	TGTTTGAATT	CCGTCGGACA	GAGGTTCCCTC	720
CATTGCTCCT	TATTTTAGAT	CGCTGTGATG	ATGCCATCAC	CCCATTGCTA	AACCAGTGGA	780
CATATCAGGC	CATGGTCCAC	GAACCTACTAG	GCATAAACAA	CAATCGGATT	GATCTTTCCA	840
GAGTGCCGGG	AATCAGTAAA	GACTTAAGAG	AAGTGGTCCT	ATCTGCTGAA	AATGATGAAT	900
TCTATGCTAA	TAATATGTAC	CTGAACCTTG	CTGAGATTGG	TAGCAATATA	AAGAATCTCA	960
TGGAAGATTT	TCAGAAGAAG	AAACCAAAAAG	AACAGCAAAA	ACTAGAATCA	ATAGCAGACA	1020
TGAAGGCGTT	TGTTGAGAAT	TATCCACAGT	TCAAGAAAAT	GTCTGGGACT	GTTTCAAAGC	1080
ATGTGACAGT	GGTTGGAGAG	CTGTCTCGAT	TGGTCAGTGA	ACGGAATCTG	CTGGAGGTTT	1140
CAGAGGTTGA	GCAAGAACTG	GCCTGTCAAA	ATGACCATTTC	TAGTGCTCTC	CAGAAATATAA	1200
AAAGGCTTCT	GCAGAACCCC	AAAGTGACAG	AGTTTGATGC	TGCCCGCCTG	GTGATGCTTT	1260
ATGCTTTACA	TTATGAGCGA	CACAGCAGCA	ATAGCCTGCC	AGGACTAATG	ATGGACCTCA	1320
GGAATAAAGG	TGTTTCTGAG	AAGTATCGAA	AGCTCGTGTC	TGCAGTTGTT	GAATATGGTG	1380
GTAAACGAGT	CAGAGGAAGT	GACCTCTTCA	GCCCCAAAGA	TGCTGTGGCT	ATCACCAAAC	1440
AATTCCCTCA	AGGACTGAAG	GGAGTAGAAA	ATGTATATAC	ACAGCATCAA	CCTTTCTCTAC	1500
ATGAAACCTT	GGATCATCTC	ATCAAAGGAA	GGCTTAAAGG	AAACCTATAT	CCTTATTTAG	1560
GCCCCAGCAC	ACTCAGAGAC	AGACCTCAGG	ATATCATTGT	GTTTGTAATT	GGAGGAGCCA	1620
CCTATGAAGA	GGCTCTAACA	GTTTATAACC	TGAACCGCAC	CACTCCTGGA	GTGAGGATTG	1680
TCCTGGGAGG	CACCACAGTG	CACAACACGA	AAAGTTTCCT	AGAGGAAGTT	CTGGCTTCTG	1740
GACTGCACAG	CCGAAGCAAG	GAGAGCTCTC	AAGTCACATC	AAGGTCAGCG	AGCAGAAGAT	1800
GAAACGGTGG	TTGGGGGAAG	GGCACAGCTT	CCTCTCTTGT	CCCCACTACA	GGTTTTCCCT	1860
ACTAAACAAA	GGTGTGGAG	AGCAGCTTTG	GGTTCTGTGC	TGGTTGTTAG	AACTCATCTC	1920
CAGGTAGCCC	ACGGATACGT	GGTTGGCACA	GACACAAGAC	TCCCAGAGTT	GTCCTAACAA	1980
TAACTCTGAG	CCCATCTCAA	CCCACTTTTC	TCCGGTAGTC	TTTATGTATC	TGTTAGCACA	2040
ATCACTTCAG	TTACTGATGA	ATTTTGTGG	GATCTGACTT	GGGGAAAGGG	TTATCAGAGC	2100
CTAGAGGGGC	TTAAAAAGTA	ATCATTTGAT	GTACATACCA	CACTCCTTGG	CTTCCTTTCT	2160
CTTCCCTTAA	CCCTTTCTGC	TTTTCATTAA	CCACATTCTT	GCACAACCTCA	TTTCTGAAAA	2220
CCTACCATGT	TTCTTTACAG	AGCCATCCAA	AAATTTTTTG	TCCCTACATA	GCAATTTTCT	2280
GTGGCACTGA	GAAACCATGT	ATGACCACAA	TAAAAATCCA	TTTTGTGAAA	GGAAAAAAA	2340
AA						2342

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: 2056691

(B) CLONE: BEP1NOT01

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Lys Ile Trp Thr Ser Glu His Val Phe Asp His Pro Trp Glu Thr  
 1 5 10 15  
 Val Thr Thr Ala Ala Met Gln Lys Tyr Pro Asn Pro Met Asn Pro Ser  
 20 25 30  
 Val Val Gly Val Asp Val Leu Asp Arg His Ile Asp Pro Ser Gly Lys  
 35 40 45  
 Leu His Ser His Arg Leu Leu Ser Thr Glu Trp Gly Leu Pro Ser Ile  
 50 55 60  
 Val Lys Ser Leu Ile Gly Ala Ala Arg Thr Lys Thr Tyr Val Gln Glu  
 65 70 75 80  
 His Ser Val Val Asp Pro Val Glu Lys Thr Met Glu Leu Lys Ser Thr  
 85 90 95  
 Asn Ile Ser Phe Thr Asn Met Val Ser Val Asp Glu Arg Leu Ile Tyr  
 100 105 110  
 Lys Pro His Pro Gln Asp Pro Glu Lys Thr Val Leu Thr Gln Glu Ala  
 115 120 125  
 Ile Ile Thr Val Lys Gly Val Ser Leu Ser Ser Tyr Leu Glu Gly Leu  
 130 135 140  
 Met Ala Ser Thr Ile Ser Ser Asn Ala Ser Lys Gly Arg Glu Ala Met  
 145 150 155 160  
 Glu Trp Val Ile His Lys Leu Asn Ala Glu Ile Glu Glu Leu Thr Ala  
 165 170 175  
 Ser Ala Arg Gly Thr Ile Arg Thr Pro Met Ala Ala Ala Phe Ala  
 180 185 190  
 Glu Lys

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: 2056691  
 (B) CLONE: BEP1NOT01

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAGCGGGGCA	GGGGCAGGTG	TAGCCTCTGT	GCCTCGTTGT	CCCCTGGCGC	TACCCGGACA	60
TCTCTCAGGG	TGCCGGCACC	ATGAAGATCT	GGACTTCGGA	GCACGTCTTT	GACCACCCGT	120
GGGAAACTGT	TACAACAGCT	GCAATGCAGA	AATACCCAAA	CCCTATGAAC	CCAAGTGTGG	180
TTGGAGTTGA	TGTGTTGGAC	AGACATATAG	ATCCCTCTGG	AAAGTTGCAC	AGCCACAGAC	240
TTCTCAGCAC	AGAGTGGGGA	CTGCCTTCCA	TTGTGAAGTC	TCTTATTGGT	GCAGCAAGAA	300
CGAAAACATA	TGTGCAAGAA	CATTCTGTAG	TTGATCCTGT	AGAGAAAACA	ATGGAACCTA	360
AATCTACTAA	TATTTCAATTT	ACAAACATGG	TTTCAGTAGA	TGAGAGACTT	ATATACAAAC	420
CACATCCTCA	GGATCCAGAA	AAAACGTGTT	TGACACAAGA	AGCCATAATT	ACCGTGAAAG	480
GAGTTAGCCT	CAGCAGTTAC	CTTGAAGGAC	TGATGGCAAG	TACGATATCC	TCAAATGCTA	540
GTAAAGGCCG	AGAAGCAATG	GAATGGGTAA	TACATAAATT	AAATGCTGAG	ATTGAAGAAC	600
TGACAGCCTC	AGCAAGAGGA	ACCATAAGGA	CTCCAATGGC	AGCAGCAGCG	TTTGCAGAGA	660
AGTGATCGTG	ACAGTTGGTA	GACAACATCG	GGTACTCCAG	GTCTCTCCAA	ACTGACTATA	720
TATTTATTTG	TTATTTTAAA	AATACAATA	TATTTTGGGT	AGTTTTTTTT	TTTTTTTTTT	780
TTGATAAGTT	GGTGAAGGC	TATGTGACTG	ATCAAAACAG	ATGCAGGGCC	TCTAAA	836

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: HEAONOT03  
 (B) CLONE: 3086794

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Glu	Ala	Leu	Ile	Leu	Glu	Pro	Ser	Leu	Tyr	Thr	Val	Lys	Ala	Ile
1				5					10					15	
Leu	Ile	Leu	Asp	Asn	Asp	Gly	Asp	Arg	Leu	Phe	Ala	Lys	Tyr	Tyr	Asp
			20					25					30		
Asp	Thr	Tyr	Pro	Ser	Val	Lys	Glu	Gln	Lys	Ala	Phe	Glu	Lys	Asn	Ile
			35				40					45			
Phe	Asn	Lys	Thr	His	Arg	Thr	Asp	Ser	Glu	Ile	Ala	Leu	Leu	Glu	Gly
			50				55				60				
Leu	Thr	Val	Val	Tyr	Lys	Ser	Ser	Ile	Asp	Leu	Tyr	Phe	Tyr	Val	Ile
65					70					75				80	
Gly	Ser	Ser	Tyr	Glu	Asn	Glu	Leu	Met	Leu	Met	Ala	Val	Leu	Asn	Cys
					85				90					95	
Leu	Phe	Asp	Ser	Leu	Ser	Gln	Met	Leu	Arg	Lys	Asn	Val	Glu	Lys	Arg
			100					105					110		
Ala	Leu	Leu	Glu	Asn	Met	Glu	Gly	Leu	Phe	Leu	Ala	Val	Asp	Glu	Ile
			115				120					125			
Val	Asp	Gly	Gly	Val	Ile	Leu	Glu	Ser	Asp	Pro	Gln	Gln	Val	Val	His
			130				135				140				
Arg	Val	Ala	Leu	Arg	Gly	Glu	Asp	Val	Pro	Leu	Thr	Glu	Gln	Thr	Val
145					150					155				160	
Ser	Gln	Val	Leu	Gln	Ser	Ala	Lys	Glu	Gln	Ile	Lys	Trp	Ser	Leu	Leu
				165					170					175	

Arg

## (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1932 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: 3086794  
 (B) CLONE: HEAONOT03

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCCAATCAG	CGGCGGCGTT	TCTTTTTCGG	CTCCACGTCG	GCACCAGCTG	CGGGGCAAGA	60
TGGAGGCGCT	GATTTTGGAA	CCTTCCCTGT	ATACTGTCAA	AGCCATCCTG	ATTCTGGACA	120
ATGATGGAGA	TCGACTTTT	GCCAAGTACT	ATGACGACAC	CTACCCAGT	GTCAAGGAGC	180
AAAAGGCCTT	TGAGAAGAAC	ATTTTCAACA	AGACCCATCG	GAATGACAGT	GAAATGCCC	240
TCTTGGAAGG	CCTGACAGTG	GTATACAAAA	GCAGTATAGA	TCTCTATTTT	TATGTGATTG	300
GCAGCTCCTA	TGAAAATGAG	CTGATGCTTA	TGGCTGTTCT	GAAGTGTCTC	TTCGACTCAT	360
TGAGCCAGAT	GCTGAGGAAA	AATGTAGAAA	AGCGAGCACT	GCTGGAGAAC	ATGGAGGGGC	420
TGTTCTTGGC	TGTGGATGAA	ATTGTAGATG	GAGGGGTGAT	CCTAGAGAGT	GATCCCCAGC	480
AGGTGGTACA	CCGGGTGGCA	TTAAGGGGTG	AAGATGTCCC	CCTTACGGAG	CAGACCGTGT	540
CTCAGGTGCT	GCAGTCAGCC	AAAGAACAGA	TCAAGTGGTC	ACTCCTTCGG	TGAAGACCTC	600
ACTGTTCCCTG	GCTCTTCATC	CTCTTCAAAA	AATTTGCATG	TCTGCTGTGA	ATTTTCATCT	660
AGTTCCCCAA	TCGATGCTCT	CAGGGTCATC	TCGGGGATCA	CAGGGATCCT	TAAATCTCCA	720
TTCTGTTTGT	GGTTGCCCCC	TCAACCTCCC	CTACACCCTT	CCTATTCTTT	TTCATTCTTC	780
TTGCAGTTCT	GGGAGTAAAG	CTCCCAGCAT	ATTTAGATAA	TAGGGCAGGG	GAAGCACCTT	840
CTTTCTTTCT	AGACTGGATT	ATGCTACAT	GCTCCCTTGC	CCTGACATTT	TTGTAATTC	900
TGTGCCCTTT	GCTGTAGCTA	CACCTCAGAT	TAAAGTAGGA	GAAAGAATGT	GCTGAGTGTT	960
TTCTCCCTTT	TGCCCTTACC	TGGCCCTCAT	CCCAACAGCC	CAGCAAGGGG	AGAGAGAAAG	1020
AGAATTCTTT	TCTATAGAAC	GAGTGGGGGC	GGGGATGGGT	AGGGATTTAT	CCAATCTAAG	1080
CCCTAACCCC	ACTTAGTGAC	CTCAGTGTTC	TCTTCCATTC	CTTCTTACTG	CCCTGTCCCTC	1140
TGCCCTGGAA	GAGGCTTTGG	GAATAGTTCA	TAGGGAAGGG	ACAACATGGA	AGAAACAGCG	1200
ATTTAAATTG	TATTGAACAG	GGCATATAAA	ATGCATTTCT	TACCCTGATC	TGGCATATAG	1260
CTTCAAAACT	GCAGTGGCGA	GTGTCCATCT	CTTAGTTAGC	TACCTTAACT	GTCCACCCCTT	1320

ACTACCTGTG	GGATCGTTGC	CTGGTTTGTC	TTCTCTGTGT	CCTGGAGCAA	AGCCAGTTCC	1380
TAAAACATAA	ACTCCATTCT	AGTCTTGGA	AGAAAAGTTT	CTACTCAGAA	CTGGGGAAGG	1440
AGTGGAACCT	ATGACTTGGG	CCTCTAGGCT	GTCTCTGTCC	CCTCAGCTCC	CCGACATGCA	1500
TTTACTCTCT	GCCGTGGGTC	TGCAGTCGCT	GCAACCTACC	CTCTCTCTGC	CTCAGCCTTA	1560
CACCCAAGCA	GTAGGTCTGT	GCTCTCCCTG	TCTCTAGGTC	GCTGAGAGAG	GTGCTTTTCT	1620
TCATAAAACC	TTTGGGGTTT	GGATTTCCCC	AGGAAGATGG	AGAATGGAAT	ACTCACTCTT	1680
GGGTCTAATC	TTTCCCCCTG	ACCCAGAACT	TCCTCCCCAC	AAAAATGCCT	TTAAAAACCT	1740
TCCTGAGACT	TAAGCATTCT	GCCCCACTTA	CTAACTGCCA	GTTCTCCAGC	ACTGAGGTGG	1800
GGCAGATAAC	TGGGCATATT	TAAGGGGGCA	TCTTTGTGTA	AAAGATGCAT	GGAGTCAGGA	1860
GAAACCACC	TTCATAACT	GCTCTGTGCA	AAGAGGAATA	AAACATTTT	TCCAAAAAAA	1920
AAAAAAAAAA	AA					1932

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: GI7703494

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Asn	Val	Val	Phe	Ala	Val	Lys	Gln	Tyr	Ile	Ser	Lys	Met	Ile	Glu
1				5					10					15	
Asp	Ser	Gly	Pro	Gly	Met	Lys	Val	Leu	Leu	Met	Asp	Lys	Glu	Thr	Thr
			20					25					30		
Gly	Ile	Val	Ser	Met	Val	Tyr	Thr	Gln	Ser	Glu	Ile	Leu	Gln	Lys	Glu
		35					40					45			
Val	Tyr	Leu	Phe	Glu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Glu	Ile	Met	Lys
	50					55					60				
His	Leu	Lys	Ala	Ile	Cys	Phe	Leu	Arg	Pro	Thr	Lys	Glu	Asn	Val	Glu
65				70						75				80	
Tyr	Leu	Ile	Gln	Glu	Leu	Arg	Arg	Pro	Lys	Tyr	Ser	Ile	Tyr	Phe	Ile
			85					90						95	
Tyr	Phe	Ser	Asn	Val	Ile	Ser	Lys	Ser	Asp	Val	Lys	Ser	Leu	Ala	Glu
			100					105					110		
Ala	Asp	Glu	Gln	Glu	Val	Val	Ala	Glu	Val	Gln	Glu	Phe	Tyr	Gly	Asp
		115					120					125			
Tyr	Ile	Ala	Val	Asn	Pro	His	Leu	Phe	Ser	Leu	Asn	Ile	Leu	Gly	Cys
	130					135					140				
Cys	Gln	Gly	Arg	Asn	Trp	Asp	Pro	Ala	Gln	Leu	Ser	Arg	Thr	Thr	Gln
145				150						155				160	
Gly	Leu	Thr	Ala	Leu	Leu	Leu	Ser	Leu	Lys	Lys	Cys	Pro	Met	Ile	Arg
			165						170					175	
Tyr	Gln	Leu	Ser	Ser	Glu	Ala	Ala	Lys	Arg	Leu	Gly	Glu	Cys	Val	Lys
			180					185					190		
Gln	Val	Ile	Ser	Lys	Glu	Tyr	Glu	Leu	Phe	Glu	Phe	Arg	Arg	Thr	Glu
		195					200					205			
Val	Pro	Pro	Leu	Leu	Leu	Ile	Leu	Asp	Arg	Cys	Asp	Asp	Ala	Ile	Thr
	210					215					220				
Pro	Leu	Leu	Asn	Gln	Trp	Thr	Tyr	Gln	Ala	Met	Val	His	Glu	Leu	Leu
225				230						235				240	
Gly	Ile	Asn	Asn	Asn	Arg	Ile	Asp	Leu	Ser	Arg	Val	Pro	Gly	Ile	Ser
			245						250					255	
Lys	Asp	Leu	Arg	Glu	Val	Val	Leu	Ser	Ala	Glu	Asn	Asp	Glu	Phe	Tyr
			260					265					270		
Ala	Asn	Asn	Met	Tyr	Leu	Asn	Phe	Ala	Glu	Ile	Gly	Ser	Asn	Ile	Lys
		275					280					285			
Asn	Leu	Met	Glu	Asp	Phe	Gln	Lys	Lys	Arg	Pro	Lys	Glu	Gln	Gln	Lys
	290					295					300				
Leu	Glu	Ser	Ile	Ala	Asp	Met	Lys	Ala	Phe	Val	Glu	Asn	Tyr	Pro	Gln
305				310						315				320	
Phe	Lys	Lys	Met	Ser	Gly	Thr	Val	Ser	Lys	His	Val	Thr	Val	Val	Gly

										325											330											335
Glu	Leu	Ser	Arg	Leu	Val	Ser	Glu	Arg	Asn	Leu	Leu	Glu	Val	Ser	Glu																	
										340											345											350
Val	Glu	Gln	Glu	Leu	Ala	Cys	Gln	Asn	Asp	His	Ser	Ser	Ala	Leu	Gln																	
										355											360											365
Asn	Val	Lys	Arg	Leu	Leu	Gln	Asn	Pro	Lys	Val	Thr	Glu	Phe	Asp	Ala																	
										370											375											380
Val	Arg	Leu	Val	Met	Leu	Tyr	Ala	Leu	His	Tyr	Glu	Arg	His	Ser	Ser																	
										385											390											395
Asn	Ser	Leu	Pro	Gly	Leu	Ile	Val	Asp	Leu	Arg	Ser	Lys	Gly	Val	Ala																	
										405											410											415
Glu	Lys	Tyr	Arg	Lys	Leu	Val	Ser	Ala	Val	Val	Glu	Tyr	Gly	Gly	Lys																	
										420											425											430
Arg	Val	Arg	Gly	Ser	Asp	Leu	Phe	Ser	Pro	Lys	Asp	Ala	Val	Ala	Ile																	
										435											440											445
Thr	Lys	Gln	Phe	Leu	Lys	Gly	Leu	Lys	Gly	Val	Glu	Asn	Val	Tyr	Thr																	
										450											455											460
Gln	His	Gln	Pro	Phe	Leu	His	Glu	Thr	Leu	Asp	His	Leu	Ile	Lys	Gly																	
										465											470											475
Arg	Leu	Lys	Glu	Asn	Leu	Tyr	Pro	Tyr	Leu	Gly	Pro	Ser	Thr	Leu	Arg																	
										485											490											495
Asp	Arg	Pro	Gln	Asp	Ile	Ile	Val	Phe	Ile	Ile	Gly	Gly	Ala	Thr	Tyr																	
										500											505											510
Glu	Glu	Ala	Leu	Thr	Val	Tyr	Asn	Leu	Asn	Arg	Thr	Thr	Pro	Gly	Val																	
										515											520											525
Arg	Ile	Val	Leu	Gly	Gly	Thr	Thr	Ile	His	Asn	Thr	Lys	Ser	Phe	Leu																	
										530											535											540
Glu	Glu	Val	Leu	Ala	Ser	Gly	Leu	His	Ser	Arg	Ser	Arg	Glu	Ser	Ser																	
										545											550											555
Gln	Ala	Thr	Ser	Arg	Ser	Ala	Asn	Arg	Arg																							
										565											570											

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 215 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: GI969170

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Gly	Lys	Tyr	Cys	Ala	Ser	Leu	Gly	Val	Leu	Lys	Gly	Pro	Trp	Asp																		
1											5											10											15
Gln	Val	Phe	Ala	Ala	Phe	Trp	Gln	Arg	Tyr	Pro	Asn	Pro	Tyr	Ser	Lys																		
										20											25											30	
His	Val	Leu	Thr	Glu	Asp	Ile	Val	His	Arg	Glu	Val	Thr	Ala	Asp	His																		
										35											40											45	
Lys	Leu	Leu	Ser	Arg	Arg	Leu	Leu	Thr	Lys	Thr	Asn	Arg	Met	Pro	Arg																		
										50											55											60	
Trp	Ala	Glu	Arg	Phe	Phe	Pro	Ala	Asn	Val	Ala	His	Asn	Val	Tyr	Ile																		
										65											70											75	
Val	Glu	Asp	Ser	Ile	Val	Asp	Pro	Lys	Asn	Arg	Thr	Met	Thr	Thr	Phe																		
										85											90											95	
Thr	Trp	Asn	Ile	Asn	His	Ala	Arg	Leu	Met	Ala	Val	Glu	Glu	Arg	Cys																		
										100											105											110	
Val	Tyr	Arg	Val	Asn	Pro	Glu	Asn	Ser	Ser	Trp	Thr	Glu	Val	Lys	Arg																		
										115											120											125	
Glu	Ala	Trp	Val	Ser	Ser	Ser	Leu	Phe	Gly	Val	Ser	Arg	Ala	Val	Gln																		
										130											135											140	
Glu	Phe	Gly	Leu	Ala	Arg	Phe	Lys	Ser	Asn	Val	Thr	Lys	Ser	Thr	Lys																		
										145											150											155	
																														160			

Gly	Phe	Glu	Tyr	Val	Leu	Ala	Arg	Met	Gln	Gly	Glu	Ala	Pro	Ser	Lys
				165					170					175	
Thr	Leu	Val	Glu	Thr	Ala	Lys	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Glu	Thr
			180				185						190		
Ala	Leu	Ala	Ala	Thr	Glu	Lys	Ala	Lys	Asp	Leu	Ala	Ser	Lys	Ala	Ala
		195					200					205			
Thr	Lys	Lys	Lys	Gln	Phe	Val									
	210					215									

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: GI441486

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Glu	Ala	Leu	Ile	Leu	Gln	Pro	Ser	Leu	Tyr	Thr	Val	Lys	Ala	Ile
1				5					10					15	
Leu	Ile	Leu	Asp	Asn	Asp	Gly	Asp	Arg	Leu	Phe	Ala	Lys	Tyr	Tyr	Asp
			20				25						30		
Asp	Thr	Tyr	Pro	Ser	Val	Lys	Glu	Gln	Lys	Ala	Phe	Glu	Lys	Asn	Ile
		35				40						45			
Phe	Asn	Lys	Thr	His	Arg	Thr	Asp	Ser	Glu	Ile	Ala	Leu	Leu	Glu	Gly
	50					55					60				
Leu	Thr	Val	Val	Tyr	Lys	Ser	Ser	Ile	Asp	Leu	Tyr	Phe	Tyr	Val	Ile
65				70					75					80	
Gly	Ser	Ser	Tyr	Glu	Asn	Glu	Leu	Met	Leu	Met	Thr	Val	Leu	Asn	Cys
			85						90					95	
Leu	Phe	Asp	Ser	Leu	Ser	Gln	Met	Leu	Arg	Lys	Asn	Val	Glu	Lys	Arg
		100					105						110		
Ala	Leu	Leu	Glu	Asn	Met	Glu	Gly	Leu	Phe	Leu	Ala	Val	Asp	Glu	Ile
	115						120					125			
Val	Asp	Gly	Gly	Val	Ile	Leu	Glu	Ser	Asp	Pro	Gln	Gln	Val	Val	His
	130					135					140				
Arg	Val	Ala	Leu	Arg	Gly	Glu	Asp	Val	Pro	Leu	Thr	Glu	Gln	Thr	Val
145				150					155					160	
Ser	Gln	Val	Leu	Gln	Ser	Ala	Lys	Glu	Gln	Ile	Lys	Trp	Ser	Leu	Leu
			165					170						175	

Arg